



SEQUENCE LISTING

<110> Skeiky, Yasin
Guderian, Jeffrey
Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding
Sequence to Facilitate Stable and High Yield Expression
of Heterologous Proteins

<130> 014058-008010US

<140> US 09/684,215
<141> 2000-10-06

<150> US 60/158,585
<151> 1999-10-07

<160> 22

<170> PatentIn Ver. 2.1

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<211> 1872
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> 32 KD serine protease MTB32A

<220>
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<222> (89)..(1156)
<223> MTB32A

<220>
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<222> (89)..(184)
<223> N-terminal hydrophobic secretory signal sequence

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<222> (185)..(1153)

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tagctacccc gacacaggag gttacggg atg agc aat tcg cgc cgc cgc tca 112
Met Ser Asn Ser Arg Arg Arg Ser
-30 -25
ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
-20 -15 -10
ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208
Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
-5 -1 1 5

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cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc	256
Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val	
10 15 20	
gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac	304
Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr	
25 30 35 40	
aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt	352
Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly	
45 50 55	
gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat	400
Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn	
60 65 70	
gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg	448
Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly	
75 80 85	
tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt	496
Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly	
90 95 100	
ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc	544
Gly Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro	
105 110 115 120	
gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg	592
Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala	
125 130 135	
gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat	640
Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp	
140 145 150	
tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat	688
Ser Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp	
155 160 165	
gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta	736
Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu	
170 175 180	
gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg	784
Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu	
185 190 195 200	
tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg	832
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
205 210 215	
atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc	880
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
220 225 230	
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	928
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
235 240 245	

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc 976
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
250 255 260

ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc 1024
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
265 270 275 280

aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt 1072
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
285 290 295

gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 1120
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
300 305 310

ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga ttctgctcg 1166
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
315 320

gataccaccc gccggccggc caattggatt ggcgccagcc gtgattgccg cgtgagcccc 1226

cgagtccgt ctcccgctgcg cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286

tcgagcacc tcccgctgcag ggcagtcacg tcgaaggcgg tgtggctcgag catccggatg 1346

ccaaggactt cggcagcgcc gccgccctgc ccgccgatcc gacctgggtt aagcacgccg 1406

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tgcgtggact catcgatcgc ctcgactacc tgcagtggct tggcatcgac tgcattcgtt 1526

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ggtttcagga gtccgcgcgc gaccagacg gaccgtacgg tgactattac gtgtggagcg 1766

acaccagcga gcgctacacc gacgcccgga tcatcttctg cgacaccgaa gagtcgaact 1826

ggtcattcga tctgtccgc cgacagttct actggcaccg attctt 1872

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<211> 355

<212> PRT

<213> Mycobacterium tuberculosis

<223> 32 KD serine protease MTB32A

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Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
35 40 45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
50 55 60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
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<210> 3
 <211> 396
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

<220>
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 <222> (1)..(396)
 <223> Ra12

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 gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg 96
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30

ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc 144
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg 192
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg 240
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg 288
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg 336
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag 384
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 gga ccc ccg gcc 396
 Gly Pro Pro Ala
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<210> 4
 <211> 132
 <212> PRT
 <213> Mycobacterium tuberculosis
 <223> 14 KD C-terminal fragment of MTB32A Ra12

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 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 Gly Pro Pro Ala
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<210> 5
 <211> 702
 <212> DNA
 <213> Artificial Sequence

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 Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro
 210 215 220

tcc gag cag ccc aac gct ccc tga gaattc 702
 Ser Glu Gln Pro Asn Ala Pro
 225 230

<210> 6
 <211> 230
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-DPPD fusion
 polypeptide

<400> 6
 Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
 130 135 140
 Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
 145 150 155 160
 Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
 165 170 175
 Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
 180 185 190
 Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
 195 200 205
 Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser
 210 215 220
 Glu Gln Pro Asn Ala Pro
 225 230

<210> 7
 <211> 1746
 <212> DNA
 <213> Artificial Sequence
 <220>
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 <222> (4)..(1740)
 <223> Ra12-WT1 fusion polypeptide

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240 245 250 255	
tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag gcg tca tcc	816
Cys Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser	
260 265 270	
ggc cag gcc agg atg ttt cct aac gcg ccc tac ctg ccc agc tgc ctc	864
Gly Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu	
275 280 285	
gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc	912
Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe	
290 295 300	
gac ggg acg ccc agc tac ggt cac acg ccc tcg cac cat gcg gcg cag	960
Asp Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln	
305 310 315	
ttc ccc aac cac tca ttc aag cat gag gat ccc atg ggc cag cag gcc	1008
Phe Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly	
320 325 330 335	
tcg ctg ggt gag cag cag tac tcg gtg ccg ccc ccg gtc tat ggc tgc	1056
Ser Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys	
340 345 350	
cac acc ccc acc gac agc tgc acc ggc agc cag gct ttg ctg ctg agg	1104
His Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg	
355 360 365	
acg ccc tac agc agt gac aat tta tac caa atg aca tcc cag ctt gaa	1152
Thr Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu	
370 375 380	
tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac	1200
Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His	
385 390 395	
agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga	1248
Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly	
400 405 410 415	
gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat	1296
Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp	
420 425 430	
gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cgg tcg gca tct	1344
Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser	
435 440 445	
gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat	1392
Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn	
450 455 460	
aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac	1440
Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His	
465 470 475	

Gly	Ala	Ser	Ala	Tyr	Gly	Ser	Leu	Gly	Gly	Pro	Ala	Pro	Pro	Pro	Ala	195	200	205
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Ser	Phe	Ile	Lys	Gln	Glu	210	215	220
Pro	Ser	Trp	Gly	Gly	Ala	Glu	Pro	His	Glu	Glu	Gln	Cys	Leu	Ser	Ala	225	230	235
Phe	Thr	Val	His	Phe	Ser	Gly	Gln	Phe	Thr	Gly	Thr	Ala	Gly	Ala	Cys	245	250	255
Arg	Tyr	Gly	Pro	Phe	Gly	Pro	Pro	Pro	Pro	Ser	Gln	Ala	Ser	Ser	Gly	260	265	270
Gln	Ala	Arg	Met	Phe	Pro	Asn	Ala	Pro	Tyr	Leu	Pro	Ser	Cys	Leu	Glu	275	280	285
Ser	Gln	Pro	Ala	Ile	Arg	Asn	Gln	Gly	Tyr	Ser	Thr	Val	Thr	Phe	Asp	290	295	300
Gly	Thr	Pro	Ser	Tyr	Gly	His	Thr	Pro	Ser	His	His	Ala	Ala	Gln	Phe	305	310	315
Pro	Asn	His	Ser	Phe	Lys	His	Glu	Asp	Pro	Met	Gly	Gln	Gln	Gly	Ser	325	330	335
Leu	Gly	Glu	Gln	Gln	Tyr	Ser	Val	Pro	Pro	Pro	Val	Tyr	Gly	Cys	His	340	345	350
Thr	Pro	Thr	Asp	Ser	Cys	Thr	Gly	Ser	Gln	Ala	Leu	Leu	Leu	Arg	Thr	355	360	365
Pro	Tyr	Ser	Ser	Asp	Asn	Leu	Tyr	Gln	Met	Thr	Ser	Gln	Leu	Glu	Cys	370	375	380
Met	Thr	Trp	Asn	Gln	Met	Asn	Leu	Gly	Ala	Thr	Leu	Lys	Gly	His	Ser	385	390	395
Thr	Gly	Tyr	Glu	Ser	Asp	Asn	His	Thr	Thr	Pro	Ile	Leu	Cys	Gly	Ala	405	410	415
Gln	Tyr	Arg	Ile	His	Thr	His	Gly	Val	Phe	Arg	Gly	Ile	Gln	Asp	Val	420	425	430
Arg	Arg	Val	Pro	Gly	Val	Ala	Pro	Thr	Leu	Val	Arg	Ser	Ala	Ser	Glu	435	440	445
Thr	Ser	Glu	Lys	Arg	Pro	Phe	Met	Cys	Ala	Tyr	Ser	Gly	Cys	Asn	Lys	450	455	460
Arg	Tyr	Phe	Lys	Leu	Ser	His	Leu	Gln	Met	His	Ser	Arg	Lys	His	Thr	465	470	475
Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Asp	Phe	Lys	Asp	Cys	Glu	Arg	Arg	Phe	485	490	495
Phe	Arg	Ser	Asp	Gln	Leu	Lys	Arg	His	Gln	Arg	Arg	His	Thr	Gly	Val	500	505	510
Lys	Pro	Phe	Gln	Cys	Lys	Thr	Cys	Gln	Arg	Lys	Phe	Ser	Arg	Ser	Asp	515	520	525
His	Leu	Lys	Thr	His	Thr	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Ser	530	535	540
Cys	Arg	Trp	Pro	Ser	Cys	Gln	Lys	Lys	Phe	Ala	Arg	Ser	Asp	Glu	Leu	545	550	555
Val	Arg	His	His	Asn	Met	His	Gln	Arg	Asn	Met	Thr	Lys	Leu	Gln	Leu	565	570	575

Ala Leu

<210> 9

<211> 672

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion

<210> 10
 <211> 220
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-human mammaglobin fusion polypeptide

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 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly
 130 135 140
 Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile
 145 150 155 160
 Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe
 165 170 175
 Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys
 180 185 190
 Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met
 195 200 205
 Gln Leu Ile Tyr Asp Ser Ser Ser Leu Cys Asp Leu Phe
 210 215 220

<210> 11
 <211> 2191
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12-H9-32A fusion
 (Ra12-MTB39-MTB32A(N-ter) fusion)

<220>
 <221> CDS
 <222> (1)..(2190)
 <223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

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 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30

atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc	144
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	192
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	240
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	288
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
85 90 95	
aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt	336
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly	
100 105 110	
gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca	384
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr	
115 120 125	
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atg gtg gat	432
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp	
130 135 140	
ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc	480
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly	
145 150 155 160	
ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg	528
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val	
165 170 175	
gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg	576
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp	
180 185 190	
ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg	624
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val	
195 200 205	
gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag	672
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln	
210 215 220	
gcc gag ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag	720
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu	
225 230 235 240	
acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt	768
Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg	
245 250 255	
gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc	816
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr	
260 265 270	

agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct 1584
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525

ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc 1632
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540

gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa 1680
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560

gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac 1728
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575

gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg 1776
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590

ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc 1824
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605

agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac 1872
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620

cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg 1920
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640

ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc 1968
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655

gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct 2016
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670

ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat tcg ctg 2064
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685

acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg 2112
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700

atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag 2160
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720

gtg gtc ggt atg aac acg gcc gcg tcc tag g 2191
 Val Val Gly Met Asn Thr Ala Ala Ser
 725 730

<210> 12

<211> 729

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Ra12-H9-32A fusion polypeptide (Ra12-MTB39-MTB32A(N-ter) fusion polypeptide)

<400> 12

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10
Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
35 40 45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
130 135 140
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145 150 155 160
Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
165 170 175
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
180 185 190
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
195 200 205
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
210 215 220
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
225 230 235 240
Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
245 250 255
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
260 265 270
Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
275 280 285
Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr
290 295 300
Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
305 310 315 320
Gly Leu Leu Glu Gln Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
325 330 335
Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
340 345 350
Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
355 360 365
Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
370 375 380
Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
385 390 395 400
Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
405 410 415

Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 13
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR amplification of Ra12 C-terminal
 fragment of MTB32A

<400> 13
 caattacata tgcatacaca tcaccatcac acggccgcgt ccgataactt c

51

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer for PCR amplification of
 Ra12 C-terminal fragment of MTB32A

<400> 14
 ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 15
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer containing enterokinase
 recognition site for PCR amplification of DPPD
 mature secreted form

<400> 15
 caattagaat tcgacgacga cgacaaggat ccacctgacc cgcacacag 48

<210> 16
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer containing enterokinase
 recognition site for PCR amplification of DPPD
 mature secreted form

<400> 16
 caattagaat tctcagggag cggtgggctg ctc 33

<210> 17
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(short)
 polypeptide

<400> 17
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 18
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12(long)
polypeptide

<400> 18

Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gly	Gln	Gly	Phe
1				5					10					15	
Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Lys	Leu
			20					25					30		
Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly	Leu	Gly	Val	Val
		35				40					45				
Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val	Val	Gly	Ser	Ala
	50					55				60					
Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val	Ile	Thr	Ala	Val
65				70					75					80	
Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala	Asp	Ala	Leu	Asn
			85					90						95	
Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Thr	Trp	Gln	Thr	Lys	Ser
			100					105					110		
Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly	Pro	Pro	Ala
		115				120						125			

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5'
oligonucleotide primer, HindIII site, for PCR
amplification of human mammaglobin

<400> 19

gcgaagctta tgaagttgct gatggtcctc atgc

34

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3'
oligonucleotide primer, XhoI site, for PCR
amplification of human mammaglobin

<400> 20

cggctcgagt taaaataaat cacaaagact gctgtc

36

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
Met His His His His His His
1 5

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:enterokinase
recognition site

<400> 22
Asp Asp Asp Lys
1